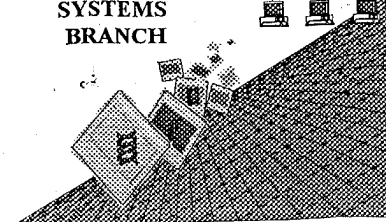


4. 4 44

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



04CO 1st
0280 cycle
5/1/01.

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/819,667
Source: OIPE
Date Processed by STIC: 4/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OTPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/819,667

DATE: 04/10/2001

TIME: 15:38:16

Does Not Comply
Corrected Diskette Needed

Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt

Output Set: N:\CRF3\04102001\I819667.raw

2 <110> APPLICANT: CANON INC.
 4 <120> TITLE OF INVENTION: Nucleic Acid Fragment Primer or Probe, and Method of
 5 Detecting Polyhydroxyalkanoate Synthesizing Microorganism by
 6 Using the Same
 8 <130> FILE REFERENCE: 4052014
 OK 10 <140> CURRENT APPLICATION NUMBER: US/09/819,667
 10 <141> CURRENT FILING DATE: 2001-03-29
 E--> 10 <160> NUMBER OF SEQ ID NOS: 9 18 in file (see below)
 12 <170> SOFTWARE: Microsoft Word

ERRORED SEQUENCES

100 <210> SEQ ID NO: 9
 101 <211> LENGTH: 30 25 shown
 102 <212> TYPE: DNA
 103 <213> ORGANISM: Artificial Sequence
 105 <220> FEATURE:
 106 <223> OTHER INFORMATION: Primer for PCR multiplication
 108 <400> SEQUENCE: 9
 E--> 109 ccaac agcgg bcayr tscag agcat 25
 199 <210> SEQ ID NO: 18
 200 <211> LENGTH: 30 last sequence in file
 201 <212> TYPE: DNA
 202 <213> ORGANISM: Artificial Sequence
 204 <220> FEATURE:
 205 <223> OTHER INFORMATION: Primer for PCR multiplication
 207 <400> SEQUENCE: 18
 208 ccaac agcgg gcatg tccag agcat 25
 E--> 212 ny_main 157155 v 1 delete at end of file

FYI: Per 1.822 of
 Sequence Rules,
 all non-coding bases
 need to be in groups
 of 10 bases each
 ==

VERIFICATION SUMMARY

DATE: 04/10/2001

PATENT APPLICATION: US/09/819,667

TIME: 15:38:18

Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt

Output Set: N:\CRF3\04102001\I819667.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:25 SEQ:9
L:212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:33 SEQ:18
L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:212 M:112 C: (48) String data converted to lower case,
L:212 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:33 SEQ:18
L:10 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (9) Counted (18)